Amendments to the Specification:

Please delete the Abstract of the Disclosure on page 1, from lines 8-20 of the specification and insert the following paragraph on a new page 105 following the claims:

-- ABSTRACT OF THE DISCLOSURE

This invention relates to newly identified polynucleotides and polypeptides, and their production and uses, as well as their variants, agonists and antagonists, and their uses. In particular, the invention relates to polynucleotides and polypeptides of a *Staphylococcus aureus* (*S. aureus*) DnaI related protein, as well as its variants, ~~hereinafter referred to as "S. aureus DnaI", "S. aureus DnaI polypeptide(s)", and "S. aureus dnaI polynucleotides" as the case may~~ be. The invention also relates to a specific interaction between the *S. aureus* DnaI related protein or specific regions thereof, and a growth-inhibitory protein encoded by the *S. aureus* bacteriophage 77 genome. The phage open reading frame (ORF) product interacts with amino acids 150 – 313 of *S. aureus* DnaI polypeptide, and the invention relates to the use of this interaction target site as the basis of drug screening assays. <u>Accordingly, the invention provides a method for the inhibition of bacterial growth, and the treatment of bacterial infection via the inhibition of DnaI.</u> --

Please replace the paragraph on page 11, lines 12-13, with the following description.

--Fig. <u>2A-2N</u> shows the complete nucleotide sequence of the *S. aureus* bacteriophage 77 genome (SEQ ID NO: 3).--

Please replace the paragraph on page 12, lines 1-7 with the following paragraph:

--Fig. <u>6A-E shows sequences and</u> alignments of *B. subtilis* DnaC sequences with the homologous sequences from *S. aureus*. 6C) shows an alignment of *B. subtilis* dnaC polynucleotide sequence (SEQ ID NO: 6) with the homologous *S. aureus* dnaC polynucleotide sequence (SEQ ID NO: 7) identified by BLAST searching the *S. aureus* database at ~~http://www.tigr.org~~ <u>The Institute of Genomic Research (TIGR) web site</u> with the *B. subtilis* dnaC sequence. 6E) shows an alignment of *B. subtilis* DnaC amino acid sequence (SEQ. ID NO: 8) with the predicted amino acid sequence of the polypeptide (SEQ ID NO: 9) encoded by the *S. aureus* dnaC polynucleotide sequence shown in Fig. 6B.--

Please replace the partial paragraph on page 45, lines 1-8 with the following paragraph:

--~~http://www.genome.ou.edu/staph.html~~ <u>The University of Oklahoma's Advanced Center for Genome Technology web site</u>. One sequence contig of 4850 nucleotides in length (Contig 981), when converted into amino acid sequence, contained within it the similar amino acid sequence GHVPELYVDNNR (SEQ ID NO: 11; Fig. 5). This tentative identification of the candidate

protein was then confirmed upon *in silico* tryptic digestion of the open reading frame found in the contig (Fig. 5). The obtained PSD/CID spectra for tryptic peptides with monoisotopic MH+ masses of 1351.8, 1412.7, and 1617.8 Da were similar to the predicted PSD/CID fragmentation patterns of the tryptic peptides with monoisotopic MH+ masses of 1351.8 and 1617.8 Da found in the contig's +3 open reading frame (Fig. 5).

Please replace the paragraph on page 46, lines 18-23 with the following paragraph:

--Databases were searched for *S. aureus* genes which may be related to the *B. subtilis* dnaC gene. Utilizing the *B. subtilis* amino acid sequence for DnaC (Accession Number P37469), a BLAST search was performed of the Staphylococcus database at ~~http://www.tigr.org~~ The Institute of Genomic Research (TIGR) web site and revealed the presence of an ORF within the *S. aureus* genome encoding a related protein. The nucleotide sequence and corresponding protein sequence are presented in Fig. 6~~AB~~ (SEQ ID NO: 7) and Fig. 6~~B~~D (SEQ ID NO: 9), respectively.--

Please replace the partial paragraph on page 84, lines 1-5 with the following partial paragraph:

--genome were sequenced at least once from both directions on two separate clones. Sequence contigs were assembled using Sequencher 3.1 software (GeneCodes) (Fig. 2). An implementation of the publicly available program SEQUIN, available for download at ~~ftp://negi.nlm.nih.gov/sequin/~~ The United States National Library of Medicine's web site, was used on phage genome sequence to identify all putative ORFs larger than 33 codons (Fig. 3). --

Please replace Table 1 on the page immediately following the claims, with the following Table 1.

--**Table 1**
Similarities in sequence between the DnaI homolog and sequences deposited in public database.

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Sequences producing significant alignments:
                                                       Score      E
                                                      (bits)   Value
gi|140025|sp|P06567|DNAI_BACSU PRIMOSOMAL PROTEIN DNAI >gi|2797...   231   5e-60
gi|468268 (M15183) ORFY [Bacillus subtilis]                        125   5e-28
gi|2072367|emb|CAA70453| (Y09255) primosomal protein DnaI [Baci...  84   1e-15
gi|530419|emb|CAA83732| (Z33058)GTP bind. CD48/PAS1/ SEC18 fam ...   67   2e-10
gi|2983431 (AE000713) DNA replication protein DnaC [Aquifex aeo...   52   4e-06
gi|1176732|sp|P45910|YQAM_BACSU HYPOTHETICAL 36.1 KD PROTEIN IN...   50   2e-05
gi|2127076|pir||I40411 hypothetical protein 5 (xre region) - Ba...   48   1e-04
gi|1722861|sp|P39782|XKDC_BACSU PHAGE-LIKE ELEMENT PBSX PROTEIN...   48   1e-04
gi|1353529 (U38906) ORF12 [Bacteriophage rlt]                       46   4e-04
gi|2983000 (AE000683) chromosome replication initiator protein ...   45   8e-04
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>gi|140025|sp|P06567|DNAI_BACSU PRIMOSOMAL PROTEIN DNAI
          >gi|279708|pir||IQBS44 dnaA protein homolog, 44K -
          Bacillus subtilis >gi|39881|emb|CAA28633| (X04963) ORF
          311 (AA 1-311) [Bacillus subtilis]
           >gi|1769996|emb|CAA99605| (Z75208) replication protein
          [Bacillus subtilis] >gi|2293281 (AF008220) DnaI
          [Bacillus subtilis] >gi|2635363|emb|CAB14858| (Z99118)
          helicase loader [Bacillus subtilis]
          Length = 311

 Score =  231 bits (583), Expect = 5e-60
 Identities = 120/280 (42%), Positives = 177/280 (62%), Gaps = 2/280 (0%)

Query: 35   DPDVKQFLEAHRAELTNAMIDEDLNVLQEYKDQQKHYDG-HKFADCPNFVKGHVPELYVD 93
            D DV+ FL+ +   +    MI++ LN L EY +Q K+      +C N ++G+ P+L V+
Sbjct: 31   DQDVQAFLKENEEVIDQKMIEKSLNKLYEYIEQSKNCSYCSEDENCNNLLEGYHPKLVVN 90

Query: 94   NNRIKIRYLQCPCKIKYDEERFEAELITSHHMQRDTLNAKLKDIYMNHRDRLDVAMAADD 153
             I I Y +CP K K D+++ +  L+ S ++Q+D L A  + + ++   RL +     D
Sbjct: 91   GRSIDIEYYECPVKRKLDQQKKQQSLMKSMYIQQDLLGATFQQVDISDPSRLAMFQHVTD 150

Query: 154  ICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIIYLPEFIRTLKGGFKD 213
              +      + KGLYLYG FG GK+F+L AIAN+L  K+  S I+Y+PEF+R LK  +D
Sbjct: 151  FLKSYNETGKGKGLYLYGKFGVGKTFMLAAIANELAEKEYSSMIVYVPEFVRELKNSLQD 210

Query: 214  GSFEKKLHRVREANILMLDDIGAEEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFDYSEL 273
             + E+KL+ V+    +LMLDDIGAE +T WVRDEVIG +L +RM +LPTFFSSNF    EL
Sbjct: 211  QTLEEKLNMVKTTPVLMLDDIGAESMTSWVRDEVIGTVLQHRMSQQLPTFFSSNFSPDEL 270

Query: 274  EHHLAMTRDGE-EKTKAARIIERVKSLSTPYFLSGENFRN 312
            +HH   ++ GE E+ KAAR++ER+  L+ P  L GEN R+
Sbjct: 271  KHHFTYSQRGEKEEVKAARLMERILYLAAPIRLDGENRRH 310


> gi|468268 (M15183) ORFY [Bacillus subtilis]
          Length = 207

 Score =  125 bits (310), Expect = 5e-28
 Identities = 67/190 (35%), Positives = 105/190 (55%), Gaps = 1/190 (0%)

Query: 20   DFXXXXXXXXXXXXXNDPDVKQFLEAHRAELTNAMIDEDLNVLQEYKDQQKHYDG-HKFAD 78
            DF             D DV+ FL+ +   +    MI++ LN L EY +Q K+      + +
Sbjct: 16   DFQNRLEQTKEKVMKDQDVQAFLKENEEVIDQKMIEKSLNKLYEYIEQSKNCSYCSEDEN 75

Query: 79   CPNFVKGHVPELYVDNNRIKIRYLQCPCKIKYDEERFEAELITSHHMQRDTLNAKLKDIY 138
            C N ++G+ P+L V+   I I Y +CP K K D+++ +  L+ S ++Q+D L A  + +
Sbjct: 76   CNNLLEGYHPKLVVNGRSIDIEYYECPVKRKLDQQKKQQSLMKSMYIQQDLLGATFQQVD 135

Query: 139  MNHRDRLDVAMAADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTII 198
            ++   RL +     D  +      + KGLYLYG FG GK+F+L AIAN+L  K+  S I+
Sbjct: 136  ISDPSRLAMFQHVTDFLKSYNETGKGKGLYLYGKFGVGKTFMLAAIANELAEKEYSSMIV 195

Query: 199  YLPEFIRTLK 208
            Y+PEF+R LK
Sbjct: 196  YVPEFVRELK 205--
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